



# 9

# SEQUENCE LISTING

<110> Allen, Keith D.  
Zhang, Qin

<120> TRANSGENIC MICE CONTAINING CX2 GENE  
DISRUPTIONS

<130> R-716

<140> US 09/900,518

<141> 2001-07-06

<150> US 60/216,178

<151> 2000-07-06

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2490

<212> DNA

<213> Mus musculus

PIPE

<400> 1

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<210> 2

<211> 764

<212> PRT

<213> Mus musculus

<400> 2

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Glu Glu Pro Asp Tyr Tyr Ser Gln Glu Leu Trp Arg Arg Gly Arg Tyr
          35          40          45
Tyr Gly His Pro Glu Pro Glu Pro Glu Pro Glu Leu Phe Ser Pro Ser
          50          55          60
Met His Glu Asp Leu Arg Val Glu Glu Gln Glu Gln Gln Glu Pro His
65          70          75          80
Gln Gln Gly His Arg Thr Pro Lys Lys Ala Ile Lys Pro Lys Lys Ala
          85          90          95
Pro Lys Arg Glu Lys Leu Val Ala Glu Thr Pro Pro Pro Gly Lys Asn
          100          105          110
Ser Asn Arg Lys Gly Arg Arg Ser Lys Asn Leu Glu Lys Ala Ala Ser
          115          120          125
Asp Asp His Gly Val Pro Val Ala His Glu Asp Val Arg Glu Ser Cys
130          135          140
Pro Pro Leu Gly Leu Glu Thr Leu Lys Ile Thr Asp Phe Gln Leu His
145          150          155          160
Ala Ser Thr Ser Lys Arg Tyr Gly Leu Gly Ala His Arg Gly Arg Leu
          165          170          175
Asn Ile Gln Ala Gly Ile Asn Glu Asn Asp Phe Tyr Asp Gly Ala Trp
          180          185          190
Cys Ala Gly Arg Asn Asp Leu His Gln Trp Ile Glu Val Asp Ala Arg
          195          200          205
Arg Leu Thr Lys Phe Thr Gly Val Ile Thr Gln Gly Arg Asn Ser Leu
210          215          220
Trp Leu Ser Asp Trp Val Thr Ser Tyr Lys Val Met Val Ser Asn Asp
225          230          235          240
Ser His Thr Trp Val Thr Val Lys Asn Gly Ser Gly Asp Met Ile Phe
          245          250          255
Glu Gly Asn Ser Glu Lys Glu Ile Pro Val Leu Asn Glu Leu Pro Val
          260          265          270
Pro Met Val Ala Arg Tyr Ile Arg Ile Asn Pro Gln Ser Trp Phe Asp
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Asn Gly Ser Ile Cys Met Arg Met Glu Ile Leu Gly Cys Pro Leu Pro
290          295          300
Asp Pro Asn Asn Tyr Tyr His Arg Arg Asn Glu Met Thr Thr Thr Asp
305          310          315          320
Asp Leu Asp Phe Lys His His Asn Tyr Lys Glu Met Arg Gln Leu Met
          325          330          335
Lys Val Val Asn Glu Met Cys Pro Asn Ile Thr Arg Ile Tyr Asn Ile
          340          345          350
Gly Lys Ser His Gln Gly Leu Lys Leu Tyr Ala Val Glu Ile Ser Asp
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His	Pro	Gly	Glu	His	Glu	Val	Gly	Glu	Pro	Glu	Phe	His	Tyr	Ile	Ala	370	375	380
Gly	Ala	His	Gly	Asn	Glu	Val	Leu	Gly	Arg	Glu	Leu	Leu	Leu	Leu	Leu	385	390	395
Leu	His	Phe	Leu	Cys	Gln	Glu	Tyr	Ser	Ala	Gln	Asn	Ala	Arg	Ile	Val	405	410	415
Arg	Leu	Val	Glu	Glu	Thr	Arg	Ile	His	Ile	Leu	Pro	Ser	Leu	Asn	Pro	420	425	430
Asp	Gly	Tyr	Glu	Lys	Ala	Tyr	Glu	Gly	Gly	Ser	Glu	Leu	Gly	Gly	Trp	435	440	445
Ser	Leu	Gly	Arg	Trp	Thr	His	Asp	Gly	Ile	Asp	Ile	Asn	Asn	Asn	Phe	450	455	460
Pro	Asp	Leu	Asn	Ser	Leu	Leu	Trp	Glu	Ala	Glu	Asp	Gln	Gln	Asn	Ala	465	470	475
Pro	Arg	Lys	Val	Pro	Asn	His	Tyr	Ile	Ala	Ile	Pro	Glu	Trp	Phe	Leu	485	490	495
Ser	Glu	Asn	Ala	Thr	Val	Ala	Thr	Glu	Thr	Arg	Ala	Val	Ile	Ala	Trp	500	505	510
Met	Glu	Lys	Ile	Pro	Phe	Val	Leu	Gly	Gly	Asn	Leu	Gln	Gly	Gly	Glu	515	520	525
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Gln	Glu	His	Thr	Pro	Thr	Pro	Asp	Asp	His	Val	Phe	Arg	Trp	Leu	Ala	545	550	555
Tyr	Ser	Tyr	Ala	Ser	Thr	His	Arg	Leu	Met	Thr	Asp	Ala	Arg	Arg	Arg	565	570	575
Val	Cys	His	Thr	Glu	Asp	Phe	Gln	Lys	Glu	Glu	Gly	Thr	Val	Asn	Gly	580	585	590
Ala	Ser	Trp	His	Thr	Val	Ala	Gly	Ser	Leu	Asn	Asp	Phe	Ser	Tyr	Leu	595	600	605
His	Thr	Asn	Cys	Phe	Glu	Leu	Ser	Ile	Tyr	Val	Gly	Cys	Asp	Lys	Tyr	610	615	620
Pro	His	Glu	Ser	Glu	Leu	Pro	Glu	Glu	Trp	Glu	Asn	Asn	Arg	Glu	Ser	625	630	635
Leu	Ile	Val	Phe	Met	Glu	Gln	Val	His	Arg	Gly	Ile	Lys	Gly	Ile	Val	645	650	655
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Gly	Val	Asn	His	Asp	Ile	Arg	Thr	Ala	Ser	Asp	Gly	Asp	Tyr	Trp	Arg	675	680	685
Leu	Leu	Asn	Pro	Gly	Glu	Tyr	Val	Val	Thr	Ala	Lys	Ala	Glu	Gly	Phe	690	695	700
Ile	Thr	Ser	Thr	Lys	Asn	Cys	Met	Val	Gly	Tyr	Asp	Met	Gly	Ala	Thr	705	710	715
Arg	Cys	Asp	Phe	Thr	Leu	Thr	Lys	Thr	Asn	Leu	Ala	Arg	Ile	Arg	Glu	725	730	735
Ile	Met	Glu	Thr	Phe	Gly	Lys	Gln	Pro	Val	Ser	Leu	Pro	Ser	Arg	Arg	740	745	750
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<212> DNA

<213> Artificial Sequence

<220>

<223> Targeting Vector

<400> 3

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<210> 4

<211> 200

<212> DNA

<213> Artificial Sequence

<220>

<223> Targeting Vector

<400> 4

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tgagcccagc caaagtcctg tggcgcctgt gttattccct agagactaca tctgagctaa 180
gttcagcttt ctctccctgc                                     200

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